

Characterization of the mRNA untranslated regions [UTR] of the *Trypanosoma cruzi* LYT1 isoforms derived by alternative *trans*-splicing

Suppl. 10. Analysis of the secondary structure and motif identification in the different 5'- and 3'- UTRs derived from *LYT1* gene. [a]. 5'UTR *mLYT1*. The **guanine rich motif** and Sxl site are indicated in gray. [b]. 5' UTR *ℓLYT1*. The **Musashi element** is indicated in gray. The **SL** in both 5'-UTR structures is indicated by a black line. [c]. *LYT1* 3' UTR-I. The Musashi binding element is indicated in gray. [d]. *LYT1*-II 3' UTR-II. The UNR site and the Musashi binding elements are indicated in gray. **The poly tail (A)** in both structures is indicated by a black line. On a scale of 0 to 1, the red color (value 1) represents a greater probability that the location of the bases in the RNA structure is real. On the other hand, the violet color (value 0) represents a low probability that the location of the bases in the structure is accurate. Structure predictions were made by the RNAalifold program, using the algorithm fold.

